ABSTRACT OF THE DISCLOSURE

The present invention relates to a method of identifying essential genes in a genome, based on an insertional mutagenesis of a population of cells or of DNA molecules and subjecting this population of cells or DNA molecules to an amplification process, whereby this total population of cells or DNA molecules which statistically represents at least one full insertionally mutated genome is amplified with at least two primer pairs and the extension products analysed, in order to distinguish essential genes from dispensable genes. The present invention is especially suited to the functional analysis of microbial genomes, and especially to haploid genomes.